

**Amendments to the Claims:**

This listing of claims will replace all prior listings of claims in the application:

**Listing of Claims:**

1. (currently amended) A hybrid polymerase having polymerase activity, wherein the polymerase comprises SEQ ID NO:23 and is at least 80% 85% identical over 700 contiguous amino acids of the *Pyrococcus furiosus* (*Pfu*) polymerase sequence set forth in SEQ ID NO: 24 ~~or at least 80% identical over 700 contiguous amino acids of the *Pyrococcus* sp. GB-D polymerase sequence set forth in SEQ ID NO:25~~, with the *proviso* that
  - (a) ~~when the polymerase is at least 85% identical to SEQ ID NO:24~~, the hybrid polymerase sequence comprises at least one hybrid position that is mutated from the native *Pfu* residue to the residue that occurs at the corresponding position of SEQ ID NO:25, wherein the hybrid position is one of the residues designated as "X" in SEQ ID NO:26; ~~or~~
  - (b) ~~when the polymerase is at least 85% identical to SEQ ID NO:25~~, the sequence comprises at least one hybrid position that is mutated from the native *Pyrococcus* sp. GB-D residue to the residue that occurs at the corresponding position of SEQ ID NO:24, wherein the hybrid position is one of the residues designated as "X" in SEQ ID NO:26.
2. (currently amended) The hybrid polymerase of claim 1, wherein the polymerase is at least 90% identical over 700 contiguous amino acids of the *Pfu* sequence set forth in SEQ ID NO:24 ~~or at least 90% identical over 700 contiguous amino acids of the *Pyrococcus* sp. GB-D sequence set forth in SEQ ID NO:25~~.
3. (currently amended) The hybrid polymerase of claim 1, wherein the hybrid polymerase comprises at least ten hybrid positions that are mutated from the native ~~reside~~ residue of SEQ ID NO:24 ~~or SEQ ID NO:25~~ to the corresponding residue of SEQ ID NO:25 ~~or SEQ ID NO:24~~.

4. (currently amended) The hybrid polymerase of claim 1, wherein the hybrid polymerase comprises at least twenty hybrid positions that are mutated from the native ~~reside~~ residue of SEQ ID NO:24 ~~or SEQ ID NO:25~~ to the corresponding residue of SEQ ID NO:25 ~~or SEQ ID NO:24~~.

5. (currently amended) The hybrid polymerase of claim 1, wherein the hybrid polymerase comprises at least forty hybrid positions that are mutated from the native ~~reside~~ residue of SEQ ID NO:24 ~~or SEQ ID NO:25~~ to the corresponding residue of SEQ ID NO:25 ~~or SEQ ID NO:24~~.

6. (currently amended) The hybrid polymerase of claim 1, wherein the hybrid polymerase comprises at least fifty hybrid positions that are mutated from the native ~~reside~~ residue of SEQ ID NO:24 ~~or SEQ ID NO:25~~ to the corresponding residue of SEQ ID NO:25 ~~or SEQ ID NO:24~~.

7. (original) The hybrid polymerase of claim 1, wherein the hybrid polymerase comprises an amino acid sequence of SEQ ID NO:2, SEQ ID NO:12, SEQ ID NO:16, or SEQ ID NO:18; or the polymerase region of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:14, or SEQ ID NO:20.

8. (original) The hybrid polymerase of claim 1, further comprising a DNA binding domain.

9. (original) The hybrid polymerase of claim 8, wherein the DNA binding domain is selected from the group consisting of Sso7d, Sac7d, and Sac7e.

10. (original) The hybrid polymerase of claim 9, wherein the DNA binding domain is Sso7d.

11. (withdrawn) The hybrid polymerase of claim 10 comprising an amino acid sequence of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:14, or SEQ ID NO:20.

12. (withdrawn) An isolated nucleic acid enclosing a hybrid polymerase as set forth in claim 1 or claim 8.
13. (withdrawn) An expression vector comprising the nucleic acid of claim 12.
14. (withdrawn) A host cell transfected with the vector of claim 13.
15. (withdrawn) An isolated nucleic acid encoding a polypeptide comprising an amino acid sequence at least 94% identical to SEQ ID NO:2, wherein the polypeptide exhibits polymerase activity.
16. (withdrawn) The isolated nucleic acid of claim 15, wherein the polypeptide comprises SEQ ID NO:2.
17. (withdrawn) The isolated nucleic acid of claim 15, wherein the nucleic acid comprises SEQ ID NO:1.
18. (withdrawn) The isolated nucleic acid of claim 15, wherein the polypeptide further comprises a DNA binding domain.
19. (withdrawn) The isolated nucleic acid of claim 18, wherein the DNA binding domain is selected from the group consisting of Sso7d, Sac7d, and Sac7e.
20. (withdrawn) The isolated nucleic acid of claim 19, wherein the DNA binding domain is Sso7d.
21. (withdrawn) The isolated nucleic acid of claim 19, wherein the nucleic acid comprises SEQ ID NO:3.
22. (withdrawn) The isolated nucleic acid of claim 19, wherein the nucleic acid encodes a polypeptide comprising SEQ ID NO:4.

23. (withdrawn) An expression vector comprising the nucleic acid of claim 15.
24. (withdrawn) A host cell transfected with the vector of claim 23.
25. (original) An isolated polypeptide, wherein the polypeptide comprises an amino acid sequence at least 94% identical to SEQ ID NO:2, and wherein the polypeptide has polymerase activity.
26. (original) The isolated polypeptide of claim 25, wherein the polypeptide comprises SEQ ID NO:2.
27. (original) The isolated polypeptide of claim 25, further comprising a DNA binding domain.
28. (original) The isolated polypeptide of claim 27, wherein the DNA binding domain is selected from the group consisting of Sso7d, Sac7d, or Sac7e.
29. (original) The isolated polypeptide of claim 27, wherein the DNA binding domain is fused to the carboxy-terminus of the polypeptide.
30. (original) The isolated polypeptide of claim 29, wherein the DNA binding domain is Sso7d.
31. (withdrawn) The isolated polypeptide of claim 30, wherein the polypeptide comprises SEQ ID NO:4.
32. (withdrawn) A method of amplifying a target sequence using a hybrid polymerase, the method comprising the steps of:  
providing a polymerase according to claim 1 or claim 25,  
combining the polymerase in an amplification reaction mixture, and  
amplifying the target sequence.